FIGURE 1. PHYTOCHROME FAMILY

prototypical phys

Cph1 (slr0473, 748 aa)

Cph2 (sll0821, 1276 aa)

Cph3 (sll1473, 481 aa)
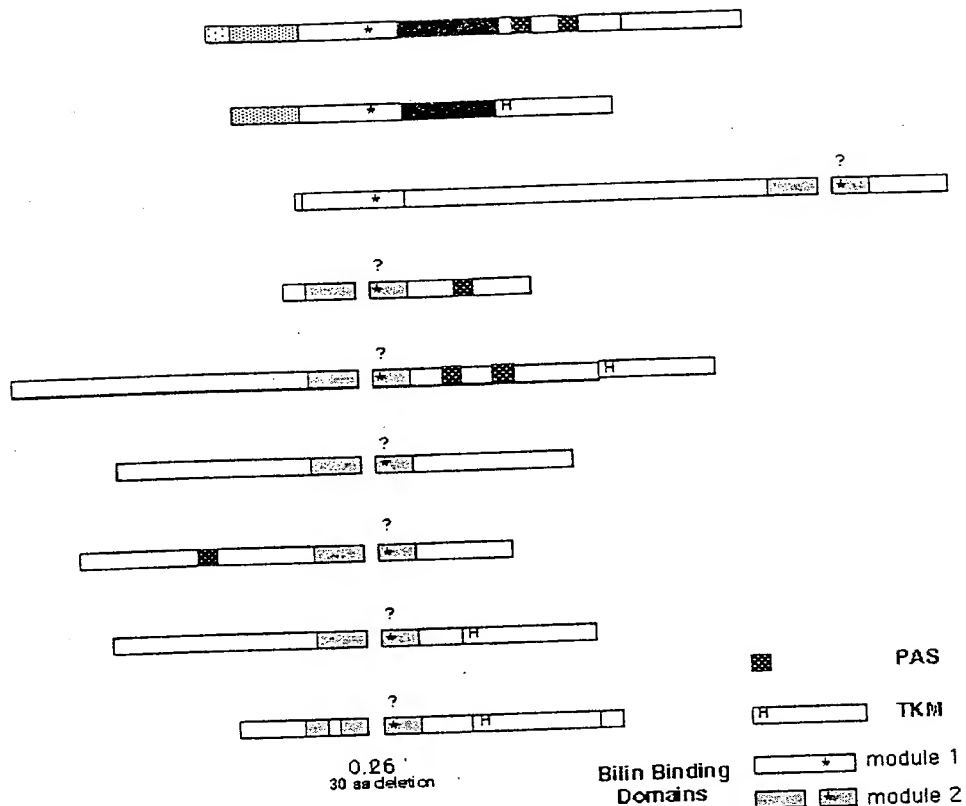
Cph4 (sll1124, 1372 aa)

Cph5 (sll0041, 891 aa)

Cph6 (slr1212, 844 aa)

Cph7 (slr1393, 950 aa)

Cph8 (slr1969, 750 aa)

0.26
30 aa deletion

■■■ PAS

[H] TKM

Bilin Binding
Domains

[　★] module 1

[　] [★] module 2

Figure 2. Phytochrome Chromophore Domain Multiple Sequence Alignment 052098

```
Atphye    1   KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHED..............................DHGEVVSEIRR-S
Atphyb    1   KLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMVYKFHED..............................EHGEVVAESKR-D
Mcphy1b   1   KLAAKAISRLQALPSGNMLLLCDALVKEVSELTGYDRVMVYKFHED..............................EHGEVIAEIRR-S
Atphyc    1   KLAAKSISRLQALPSGSMERLCDTMVQEVFELTGYDRVMAYKFHED..............................GHGEVIAECCR-E
Atphya    1   KLAAKAITRLQSLPSGSMERLCDTMVQEVFELTGYDRVMAYKFHED..............................DHGEVVSEVTK-P
Slr0473   1   HMANAALNRLR..QQANLRDFYDVIVEEVRRMTGFDRVMLYRFDEN..............................NHGDVIAEDKR-D
Sll1473   1   RFINQITQHIR..QSLNLETVLNTTVAEVKTLLQVDRVLIYRIWQD..............................GTGSAITESVN-A
Pcae      1   EDFSEVTLKIR..QSLQLKEILHTTVTEVQRILQADRVLIYHVLPD..............................GTGKTISESVL-P
Slr1212   1   SLLREITQRIR..ASLNINDILYSTVTEVARQFLNTDRVVLFKFNSQ.............................SDFSVGNIVAESVL-A
Sll0821b  1   KLVLKIANKIR..ASLKLETILRTTVTEVARTIHADRVLIHHIQED.............................WSGDVVTESHN-D
Sll1124   1   KLLSSISQRIR..ESLKLETILRTTVTEVARTIHADRVLIHHIQED............................GLGTTIAESVV-N
Sll0041   1   QILKELTLKIS..AAINSEQVFDIAAQEIRLALKADRVIVYRFDAT............................WAGTVIVESVA-E
Slr1393   1   RALTRVIEGIR..QTLELQNIFRATSDEVRHLLSCDRVLVIYQFHYSQPSLTPLEENQIPAPRPRQQYGEVTYEARRSP
Sll1069   1   KLLSQVIAQIR..QSLQLSEILNNAVTAVQKFLFVDRLVIYKFASD............................GSGEVLAEAVNRA
Sll0821a  1   DFLRNVINKFH..RALTLRETLQVIVEEARIFLGVDRVKIYKFASD..............................
```

```
Atphye    59  DLEPYIGLHYPATDIPQAARFLFKQNRVRMICDGNATPVKVVQ..SEELKRPLCLVNSTLRAPHGGHTQYMANMGSVA
Atphyb    59  DLEPYIGLHYPATDIPQASRFLFKQNRVRMIVDGNATPVLVVQ..DDRLTQSMCLVGSTLRAPHGGHSQYMANMGSIA
Mcphy1b   59  DLEPYIGLHYSATDIPQASRFLFMRNKVRMICDCSAPVKVVQ..DKSLSQPISLSGSTLRAPHGCHAQYMSNMGSVA
Atphyc    59  DMEPYIGLHYSATDIPQAARFLFMKNKVRMIVDCNAKHARVLQ..DEKLSFDLTLCGSTLRAPHSCHLQYMANMDSIA
Atphya    59  GLEPYIGLHYPATDIPQAARFLFIHNPIRVIPDVYGAVPLTPAVNPSTNRAVDLTESILRSAYHCHLTYLKNMGVGA
Slr0473   57  DMEPYIGLHYPESDIPQPARRLFIHNPIRVI.........EYHQAYTK..GKVR.....AINDIDQ..DDIEICLADFVKQFGVKS
Sll1473   57  NYPSILGRTFSDEVFRV...................EYQQLYAQ..GRVR.....AIADVHDPTAGLAECLVEFVDQFHIKA
Pcae      57  DYPTLMDLEFPQEVFPQ...................NYAQRYQQ..GRID.....VIEDIHQ..SHLRQCHIDFLARLQVRA
Slr1212   60  PFKPIINSAIEETCFSN..................HYLRLYRE..GRVR.....AVSDIEK..ADLAQCHKELLRHYQVKA
Sll0821b  57  FCRSIINDEIDDPCFKG..................ECYQRYLN..GYIY.....ASRD..QLPDCAINCAVQCFTVAESQS
Sll1124   57  GQPSVMQMDLSPESFPP..................SYVEKYRS..GRIQ.....ATRDIYN..AGLTPCHIGQLKPFEVKA
Sll0041   57  GYPKALGATIADPCFAD..................TYLQENEG..GRYRNHESLAVGDVE..TAGFTDCHLDNLRRFEIRA
Slr1393   57  MWEPLKDLQNNFPLWQD..................VFSYEQKYLK..GAV.....VAVSDIENHYSS..SYCLVGLLQRYQVRA
Sll1069   57  EIDTMLGIMTENDCFSQ..................SHELSGRISPTEHSNGHYTTVDSCHIQYLLAMGVLS
Sll0821a  58  ALPSLLGLHFPVEDIPPQAREELGNQRKMIAVDVAHRRKK..SHELSGRISPTEHSNGHYTTVDSCHIQYLLAMGVLS
```

```
Atphye    135  SDALAIVVKGKD.....................SSKLWGLVVGHHCSPRYVPFPLRYACEF.LMQAFGLQLQMELQLASQLAEK
Atphyb    135  SLIAMAVINGNEDDGSNVASG..........RSSMRLWGLVVCHHTSSRCIPFPLRYACEF.LMQAFGLQLNMELQLALQMSEK
Mcphy1b   135  SLVMAVIINDNSSEEGATAAGGILHKGRKLWGLVVCHHASPRFVPFPLRYACEF.LTQVFGVQINKEAESAVELKEK
Atphyc    135  SLVMSVTINGSDSDEMNRD.....LQTGRHLWGLVVCHNTTPRFVPFPLRYACEF.FGRVVFSNISAQEDTETFDYRV
Atphya    135  SLVMAVVVNEEDGEGDAPDATTQPQKRKRLWGLVVCHHTTPRFVPFELRKACEF.RPWQPWEVELMKQLANQVAIAIQQSEYEQL
Slr0473   111  KLVVPILQHNRASSLDNESEFPY.......LWGLLITHQCAFT....RPWQPWEVELMKQLANQVAIAIQQSEYEQL
Sll1473   111  KLIVPIVQNLNANSQNQ..........LWGLLCIHQCDSV....RQWVDFELELMQQLADQISIALSQAQELGRL
Pcae      113  NLVLPLINDAI................LWGLLIAHECKTP....RYWQEEDLQLLMELATQVAIAIQQSLEYEQA
Slr1212   114  NLVVPVVFNEN................LWGLLIVHQCSSS....RTWQTAEIQLMQSLGNQLAIAIQQSLEYERL
Sll0821b  111  RIVAPIVFDHS................LLGLLAHQCGSP....RDWHQNEIDLFGQLTVQVGLALERSDLAQQ
Sll1124   111  NLVAPINYKGN................LWGLLGAYQNGAP....RHWQAREIHDLHQIANQLGVAVYQAQELARF
Sll0041   116  FLTVPVFVGEQ................LWGLLIAHQCHHP....RQWLDSEKNFLGQIGEHLAVAIVQSLLYSEV
Slr1393   134  KLVAPIIVEGQ................LWGIMAVHHSK-P....RRFTEQEWETMALLSKEVSLAITQSQLSRQV
Sll1069   134  SLTVPVMQDQQ................
```

CONSTRUCT AND AMINO ACID SEQUENCE OF Cph2-N197-ST

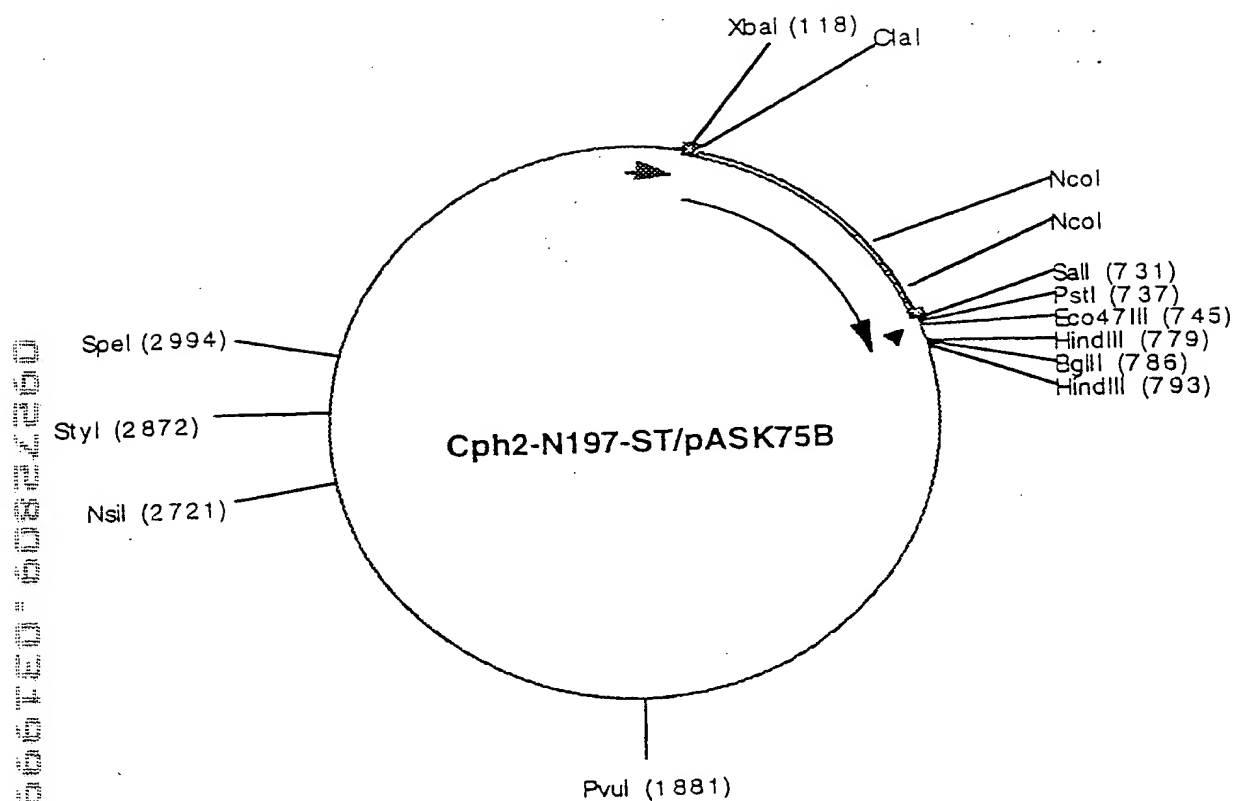Figure 3A

SEQ. ID NO: 9
Cph2-N197__ peptide sequence

MNPNRSLEDF LRNVINKFHR ALTLRETLQV IVEEARIFLG VDRVKIYKFA

SDGSGEVLAE AVNRAALPSL LGLHFPVEDI PPQAREELGN QRKMIAVDVA

HRRKKSHELS GRISPTEHSN GHYTTVDSCH IQYLLAMGVL SSLTVPVMQD

QQLWGIMAVH HSKPRRFTEQ EWETMALLSK EVSLAITQSQ LSRQVHQGRP

AGSAWRHPQF GG
    Strep-tag

Figure 3B